



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105120

TO: Nita M Minnifield
Location: REM-3C01-3C18
Art Unit: 1645
Tuesday, October 19, 2004

Case Serial Number: 10/034623

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
12/15/04*

135120

STIC-Biotech/ChemLib

From: Minnifield, Nita
Sent: Friday, October 15, 2004 8:41 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

10/034623

STIC

Please do a commercial and interference sequence search on SEQ ID NO: 6 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: *10/18/04*
Date Completed: *10/11/04*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *CDP*
WWW/Internet: _____
Other(Specify): _____

OM protein - protein search, using sw model

Run on: October 18, 2004, 14:39:24 ; Search time 40 Seconds (without alignments)

Title: US-10-034-623-6
Perfect score: 1357
Sequence: 1 MIGIEGGRGDMSENVFACV. RPAAGRKTPGARRAGAKR 269

Scoring table: BLOSUM62
Scorched: 283416 seqs, 98216763 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
GapOp 10.0 , Gapext 0.5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
1	1357	100.0	269	T31309 histone H1 DNA binding protein
2	220.5	16.0	223	A36884 histone H1 homolog
3	219	16.1	207	G81715 Hc2 nucleoprotein
4	217	16.0	207	A41936 histone H1 homolog
5	204	15.0	203	D71563 probable histone-1 histone-like protein
6	203.5	15.0	172	F72083 histone-like protein
7	203.5	15.0	172	F86538 histone-like protein
8	201	14.8	328	S01359 salivary glue protein
9	199.5	14.7	182	S61926 histone H1 homolog
10	174	12.8	165	JN0853 histone homolog 2 histone-like DNA binding protein
11	169	12.5	218	JN0853 histone homolog 2 histone-like DNA binding protein
12	154	11.3	1390	SS1364 sperm tail-specific histone H1, gonadal histone H1, (clone)
13	153	11.3	248	HSUR1P histone H1, (clone)
14	152.5	11.2	288	SS5302 histone H1, (clone)
15	151.5	11.2	1052	A44937 kinetoplast-associated protein
16	151.5	11.2	1701	T09127 histone H1-III
17	148	10.9	135	S2 T09127 histone H1-III
18	148	10.9	2	S44152 histone H1 - Buplo histone H1-III
19	145.5	10.5	211	A28100 histone H1-beta, e histone H1 - commo
20	142.5	10.5	282	S55302 histone H1 (clone)
21	142.5	10.5	284	T02421 histone H1 - (clone)
22	140.5	10.4	241	JN0748 histone H1-III - Vo probable translati
23	139	10.2	1403	2 T11583 histone H1 - fruit
24	138.5	10.2	384	2 B43592 outer membrane protein
25	138.5	10.2	1773	2 A81937 histone H1-beta, e
26	138.5	10.2	1815	2 C81169 IGA-specific metal
27	136.5	10.1	421	2 JV0057 tolla protein - Esc histone H1 - fruit
28	136	10.0	289	2 S07371 conserved hypothetical protein
29	136	10.0	289	2 C81203

RESULT 1

131309 histone H1 DNA binding protein - Cenarchaeum symbiosum
 C;Species: Cenarchaeum symbiosum
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T31309
 R;Schleper, C.; Delong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
 J;Bacteriol. 180, 5003-5009, 1998
 A;Title: Genomic analysis reveals chromosomal variation in natural populations of the
 A;Reference number: Z20594; MUID:98422450; PMID:9748430
 A;Accession: T31309
 A;Status: preliminary; translated from GB/ENBL/DBJ
 A;Molecule type: DNA
 A;Residue: 1-269 <SCH>
 A;Cross-references: UNIPROT:074057; EMBL:AF083072; NID:93599393; PID:93599395; PIDN:AU
 A;Gene: hc2

Query Match 100.0%; Score 1357; DB 2; Length 269;
 Best Local Similarity 100.0%; Prod. No. 1.7e-86;
 Matches 269; Conservative 0; Mis matches 0; Indels 0; Gaps 0;

Matches 269; Conservative 0; Mis matches 0; Indels 0; Gaps 0;

QY 1 MHGTEGGGRGMSENIVFAVFCVACARGVTKDEMKYTDGRVFKECHRRHGGQIRFPNPEVEQ 60
 1 MHGTEGGGRGMSENIVFAVFCVACARGVTKDEMKYTDGRVFKECHRRHGGQIRFPNPEVEQ 60

QY 61 RVEAEKVDLITQMRNQLAENRASGGGGVHSATSAEAEQHRAELKQVQVQWENQLAEN 120
 61 RVEAEKVDLITQMRNQLAENRASGGGGVHSATSAEAEQHRAELKQVQVQWENQLAEN 120

QY 121 RKAAGKPARKKAAGTARKSGKETVVRKTKGTRTAGKQAGARKRTVKTARTRXTAKKA 180
 121 RKAAGKPARKKAAGTARKSGKETVVRKTKGTRTAGKQAGARKRTVKTARTRXTAKKA 180

QY 181 AGRKAGARRKATVKVTKIGRKTRKTTARRTAGKSTVVRKSTVVRKTKGCKAVRR 240
 181 AGRKAGARRKATVKVTKIGRKTRKTTARRTAGKSTVVRKSTVVRKTKGCKAVRR 240

QY 241 KSTVVRTRARRPAGKTPGAAARRAGAKER 269
 241 KSTVVRTRARRPAGKTPGAAARRAGAKER 269

RESULT 2

A3884 histone H1 homolog Hc2 - Chlamydia trachomatis
 C;Species: Chlamydia trachomatis
 C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A3884; JN0851
 R;Brickman, T.J.; Barry III, C.E.; Hackstadt, T.
 J;Bacteriol. 175, 4274-4281, 1993

OM protein - protein search, using sw model

Run on: October 18, 2004, 14:28:24 ; Search time 132 seconds

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Title: US-10-034-623-6

Perfect score: 1357

Sequence: 1 MFGIEGGRGDMSENVFACV. RPAAGRKTPGRAARRAGAKER 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_5_ptodata/2/pubpaa/us07_PUBCOMB.pep:*

2: /cgn2_6_ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6_ptodata/2/pubpaa/us06_NEW_PUB.pep:*

4: /cgn2_6_ptodata/2/pubpaa/us05_PUBCOMB.pep:*

5: /cgn2_6_ptodata/2/pubpaa/us07_NEW_PUB.pep:*

6: /cgn2_6_ptodata/2/pubpaa/PCTRS_PUBCOMB.pep:*

7: /cgn2_6_ptodata/2/pubpaa/us08_NEW_PUB.pep:*

8: /cgn2_6_ptodata/2/pubpaa/us08_PUBCOMB.pep:*

9: /cgn2_6_ptodata/2/pubpaa/us09A_PUBCOMB.pep:*

10: /cgn2_6_ptodata/2/pubpaa/us05_PUBCOMB.pep:*

11: /cgn2_6_ptodata/2/pubpaa/tr09C_PUBCOMB.pep:*

12: /cgn2_6_ptodata/2/pubpaa/us09_NEW_PUB.pep:*

13: /cgn2_6_ptodata/2/pubpaa/us09A_PUBCOMB.pep:*

14: /cgn2_6_ptodata/2/pubpaa/us09_PUBCOMB.pep:*

15: /cgn2_6_ptodata/2/pubpaa/us09C_PUBCOMB.pep:*

16: /cgn2_6_ptodata/2/pubpaa/us10_PUBCOMB.pep:*

17: /cgn2_6_ptodata/2/pubpaa/us10_NEW_PUB.pep:*

18: /cgn2_6_ptodata/2/pubpaa/us60_PUBCOMB.pep:*

19: /cgn2_6_ptodata/2/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1357	100.0	269	13 US-10-027-806-6 Sequence 6, Appli
2	1357	100.0	269	13 US-10-034-623-6 Sequence 6, Appli
3	1357	100.0	269	14 US-10-029-120-6 Sequence 6, Appli
4	1357	100.0	269	14 US-10-156-761-9889 Sequence 6, Appli
5	208	15.3	376	14 US-10-156-761-9889 Sequence 9889, Appli
6	204	15.0	203	10 US-09-820-843A-7 Sequence 7, Appli
7	203.5	15.0	172	10 US-09-820-843A-5 Sequence 5, Appli
8	203.5	15.0	182	15 US-10-289-7624402 Sequence 402, Appli
9	177	13.0	217	14 US-10-156-761-10221 Sequence 10221, Appli
10	160.5	11.8	355	14 US-10-156-761-13658 Sequence 13658, Appli
11	159.5	11.8	329	15 US-10-282-122A-67699 Sequence 67699, Appli
12	155.5	11.5	212	15 US-10-282-122A-61735 Sequence 61735, Appli
13	154	11.3	969	15 US-10-282-122A-50758 Sequence 50758, Appli
14	152.5	11.2	301	16 US-10-437-963-182491 Sequence 182491, Appli

```

15: /cgn2_6/ptodata/2/pubpaa/us60_pubcomb.pep:*
16: /cgn2_6/ptodata/2/pubpaa/us60_pubcomb.pep:*
17: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB_PEP:*
18: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB_PEP:*
19: /cgn2_6/ptodata/2/pubpaa/us60_pubcomb.pep:*

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SUMMARIES

No.	Score	Match	Length	DB	ID	Description
-----	-------	-------	--------	----	----	-------------

RESULT 1

US-10-027-806-6

; Sequence 6, Application US/10027806

; Publication No. US20020160476A1

GENERAL INFORMATION:

APPLICANT: Swanson, Ronald V.

APPLICANT: Feldman, Robert A.

APPLICANT: Schieber, Christa

TITLE OF INVENTION: NUCLEAR ACIDS AND PROTEINS FROM CENARCHAUM SYMBIOSUM

FILE REFERENCE: DCCP-002A

CURRENT APPLICATION NUMBER: US/10-027-806

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408, 020

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 6

LENGTH: 269

TYPE: PRT

ORGANISM: Cenarchaeum symbiosum

US-10-027-806-6

15 149.5 11.0 289 16 US-10-437-963-144785 Sequence 144785,
16 148 10.9 223 13 US-10-051-643-201 Sequence 201, App
17 148 10.9 223 14 US-10-205-979-52 Sequence 52, Appl
18 148 10.9 1387 14 US-10-156-761-13000 Sequence 13000, A
19 147.5 10.9 260 16 US-10-437-963-10671 Sequence 107671,
20 146.5 10.8 366 14 US-10-156-761-10482 Sequence 10892, A
21 145.5 10.7 184 15 US-10-424-599-188977 Sequence 188977,
22 140 10.3 337 16 US-10-437-963-157680 Sequence 157680,
23 139 10.2 16608 15 US-10-084-86A-8 Sequence 8, Appl
24 138.5 10.2 428 15 US-10-282-122A-55748 Sequence 55748, A
25 138.5 10.2 446 16 US-10-437-963-177362 Sequence 127362,
26 138.5 10.2 1773 15 US-10-282-122A-55817 Sequence 65817, A
27 138 10.2 279 14 US-10-181-071-7 Sequence 7, Appl
28 137.5 10.1 942 14 US-10-156-761-12155 Sequence 12155, A
29 137 10.1 2263 14 US-10-408-761-2231 Sequence 2231, Ap
30 136.5 10.1 421 15 US-10-282-122A-56483 Sequence 56483, A
31 136 10.0 211 16 US-10-437-963-124659 Sequence 174659,
32 136 10.0 228 14 US-10-156-761-9425 Sequence 9425, Ap
33 136 10.0 321 9 US-09-864-761-33718 Sequence 33718, A
34 136 10.0 361 9 US-09-064-761-33614 Sequence 33614, A
35 136 10.0 361 9 US-09-064-761-34141 Sequence 34141, A
36 136 10.0 1047 14 US-10-029-386-33522 Sequence 33522, A
37 136 10.0 1087 14 US-10-029-386-33407 Sequence 32407, A
38 135.5 10.0 202 16 US-10-437-963-153886 Sequence 163886,
39 135.5 10.0 204 16 US-10-437-963-111115 Sequence 111115,
40 135.5 10.0 838 14 US-10-156-761-10342 Sequence 10342, A
41 135 9.9 221 15 US-10-424-599-22204 Sequence 252204,
42 134.5 9.9 315 16 US-10-437-963-20938 Sequence 20938,
43 134.5 9.9 503 15 US-10-282-122A-50517 Sequence 50517, A
44 134 9.9 251 16 US-10-417-963-180341 Sequence 180341,
45 134 9.9 309 16 US-09-820-843A-24 Sequence 24, Appl

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: October 18, 2004, 14:19:22 ; Search time 40 Seconds (without alignments)

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 65318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:*

- 1: /cgn2_6/ptcdata/1/iaa/5A_COMBO_PEP:*
- 2: /cgn2_6/ptcdata/1/iaa/5B_COMBO_PEP:*
- 3: /cgn2_6/ptcdata/1/iaa/6A_COMBO_PEP:*
- 4: /cgn2_6/ptcdata/1/iaa/6B_COMBO_PEP:*
- 5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMBO_PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	269	4	US-09-408-020-6
2	203.5	100.0	182	4	US-09-198-452A-402
3	148	10.9	223	3	US-09-095-815-201
4	148	10.9	223	4	US-09-205-446-201
5	147	10.8	246	4	US-09-252-991A-16586
6	137.5	10.1	492	4	US-09-252-991A-28339
7	135.5	10.0	315	4	US-09-252-991A-0553
8	8	9.8	214	3	US-09-041-889-27
9	132.5	9.8	214	4	US-09-417-264-27
10	132.5	9.8	443	4	US-09-252-991A-26132
11	132	9.8	722	4	US-09-252-991A-24102
12	132	9.7	434	1	US-09-097-830E-3
13	132	9.7	434	2	US-08-456-112B-3
14	132	9.7	1523	4	US-09-538-092-955
15	130.5	9.6	491	4	US-09-489-039A-7836
16	130.5	9.6	726	4	US-09-392-714-21
17	130	9.5	536	4	US-09-252-991A-16754
18	129.5	9.5	212	4	US-09-490-039A-13074
19	129.5	9.5	437	4	US-09-252-991A-26942
20	129	9.5	469	4	US-09-489-039A-13565
21	129	9.5	283	4	US-09-270-767-39894
22	129	9.5	283	4	US-09-270-767-55111
23	128.5	9.5	543	4	US-09-252-991A-31103
24	128	9.4	195	4	US-09-252-991A-25427
25	127.5	9.4	561	4	US-09-252-991A-23080
26	127.5	9.4	757	4	US-09-252-991A-23569
27	127.5	9.4	1213	3	US-09-411-814-76

ALIGNMENTS

RESULT 1	
US-09-408-020-6	US-09-408-020-6
Query Match	100.0%; Score 1357; DB 4;
Best Local Similarity	100.0%; Pred. No. 2.6e-137;
Matches	269; Conservatory 0; Mismatches 0;
Qy	1 MHEGIEGRGDMSENIVAFACVACAGRTKDEMKYVGRVFRH
Db	1 MHEGIEGRGDMSENIVAFACVACAGRTKDEMKYVGRVFRH
Qy	61 RVALKVDLQIMRNQLAEMNRASGDDGVISSATSAEAEDE
Db	61 RVALKVDLQIMRNQLAEMNRASGDDGVISSATSAEAEDE
Qy	121 RKAPEKPKARAKTARRSKGKVKRKGKTAGKKG
Db	121 RKAPEKPKARAKTARRSKGKVKRKGKTAGKKG
Qy	181 AGRKAGARRKAKTARRSKGKVKRKGKTAGKKG
Db	181 AGRKAGARRKAKTARRSKGKVKRKGKTAGKKG
Qy	241 KSTVKTARRPAGKTPGKARRAGKRR
Db	241 KSTVKTARRPAGKTPGKARRAGKRR
RESULT 2	US-09-18-452A-402

Sequence	22853, A
Sequence	16592, A
Sequence	28514, A
Sequence	36084, A
Sequence	51301, A
Sequence	23613, A
Sequence	32957, A
Sequence	30531, A
Sequence	28386, A
Sequence	32991, A
Sequence	26999, A
Sequence	20210, A
Sequence	30909, A
Sequence	25637, A
Sequence	36681, A
Sequence	1898, A
Sequence	28125, A
Sequence	21789, A

GenCore version 5.1.6
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OM protein - protein search, using sw mode1

Run on: October 18, 2004, 14:30:38

; Search time 160 Seconds
 (without alignments)

603.114 Million cell updates/sec

Title: US-10-034-623-6
 Perfect score: 1357

Sequence: 1 MHGEGGRGDMSENVFAFCV.....RPAQKTPGRAARRAGAKRR 269

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseqp_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1357	100.0	269	3 AAY90914
2	226	95	2 AAY37179	Cenarchaeae
3	204	15.0	7 ABO23506	Protein i
4	203.5	15.0	172 ABO23504	Abob23506 Chlamydop
5	15.0	182	2 AAY34984	Chlamydop
6	159.5	11.8	329 ABO39775	Amino aci
7	11.5	212 ABO33811	Abus39775 Protein e	
8	154	11.3	6 ABO23234	Abu33811 Protein e
9	153	11.3	2 AAY138633	Abu23234 Protein e
10	151.5	11.2	540 ADO1917	Ray8693 Neisseria
11	148	10.9	2 AAY19228	Adm1917 Protein e
12	148	10.9	223 ABO7903	Aay19228 Amino aci
13	147	10.8	246 ABO67840	Abp07903 Mycobacte
14	146	10.8	7 ABO67897	Abob7840 Pseudomon
15	145.5	10.7	583 ABO69005	Aay74897 Neisseria
16	144.5	10.6	267 AAY38692	Abg9005 Novel hum
17	144.5	10.6	2 AAY78892	Aay8692 Neisseria
18	141	10.4	1275 ABO20340	Aay78892 Neisseria
19	140	10.3	289 ABO80336	Abg0340 Novel hum
20	139	10.2	467 ABO65558	Abp0336 N. gonorr
21	139	10.2	4 ABO20365	Abp65558 Human pol
22	138.5	10.2	428 ABO21824	Abg0365 Novel hum
23	138.5	10.2	1773 ABO17893	Abu21824 Protein e
24	138	10.2	279 AAU03592	Abi17893 Protein e
25	467	4 AAB03592	Aau03592 Human DNA	
				Aab94309 Human pro

Aay96808 Neisseria
 Abt79593 Pseudomon
 Aay74898 Neisseria
 Abo53053 Human put
 Adj7425 Human hea
 Abu8559 Neisseria
 Aay8690 Neisseria
 Aam1401 Peptide #
 Abb32946 Peptide #
 Aam26407 Peptide #
 Abb2775 Human pep
 Abb8420 Protein #
 Aam66130 Human bon
 Aam53747 Human bra
 Abg47798 Human liv
 Aam01742 Peptide #
 Abg35780 Human Pep
 Aam4436 Peptide #
 Aam13889 Peptide #
 Abb32834 Peptide #

Aay74897 Neisseria
 Abt79593 Pseudomon
 Aay74898 Neisseria
 Abo53053 Human put
 Adj7425 Human hea
 Abu8559 Neisseria
 Aay8690 Neisseria
 Aam1401 Peptide #
 Abb32946 Peptide #
 Aam26407 Peptide #
 Abb2775 Human pep
 Abb8420 Protein #
 Aam66130 Human bon
 Aam53747 Human bra
 Abg47798 Human liv
 Aam01742 Peptide #
 Abg35780 Human Pep
 Aam4436 Peptide #
 Aam13889 Peptide #
 Abb32834 Peptide #

RESULT 1
 ID AAY90914 standard; protein; 269 AA.
 XX
 AC AAY90914;
 XX
 DT 30-AUG-2000 (first entry)
 XX
 DE Cenarchaeum symbiosum open reading frame protein sequence SEQ ID NO:6.
 XX
 KW Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology;
 KW characterisation; archae; therapeutic; industrial; laboratory.
 XX
 OS Cenarchaeum symbiosum.
 XX
 PN WO20018909-A2.
 XX
 PD 06-APR-2000.
 XX
 PR 29-SEP-1999; 99WO-US022752.
 XX
 PR 29-SEP-1998; 98US-0102294P.
 XX
 PA (DIVE-) DIVERSA CORP.
 XX
 PI Swanson RV, Feldman RA, Schleper C;
 XX
 DR WPI: 2000-293148/25.
 DR -PSSB; AAS45189.
 XX
 PT New nucleic acids and proteins isolated from the non-thermophilic
 PT crenarchaeote Cenarchaeum symbiosum, useful in characterizing the
 PT physiology of these archae and in therapeutic, industrial or laboratory
 PT techniques.
 XX
 PS Claim 24; Page 111-112; 210pp; English.

PT New nucleic acids and proteins isolated from the non-thermophilic
 PT crenarchaeote Cenarchaeum symbiosum, useful in characterizing the
 PT symbiosum. The nucleic acids and proteins identified in the present
 PT invention are useful in characterising the physiology of these archae and
 PT can be used in therapeutic, industrial or laboratory techniques. AAS45227
 CC to AAS5260 represent promoter sequences from Cenarchaeum symbiosum.
 CC AAS5261 to AAS5269 represent PCR primers and probes used in examples
 CC from the present invention
 XX
 SQ Sequence 269 AA;